#5

SEQUENCE LISTING

<110> Rafalski, J. Antoni
Cahoon, Rebecca E.
Coughlan, Sean
Miao, Guo-Hua

<120> PLANT VITAMIN E BIOSYNTHETIC ENZYMES

<130> BB-1289

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<141> 2002-01-14

<150> PCT/US99/28588
<151> 1999-12-02

<150> 60/110,781
<151> 1998-12-03

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catcaaattc accatcatca cctgtcgcaa gcctggagcc gcgtangagg aggcaaggag 600
cacaagttac tagcacagca caggatgcaa gtgcatatgt agatcatggc acatcgccgt 660
cactcatcat actgcacaaa atcaaatctc caggacattt aataattctg cacctcanat 720
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Pro Phe Pro Asp Gly Gln Phe Asp Leu Val Trp Ser Met Glu Ser Gly
35 40 45

Glu His Met Pro Asp Lys Arg Lys Phe Val Ser Glu Leu Ala Arg Val
50 55 60

Ala Ala Pro Gly Gly Thr Ile Ile Ile Val Thr Trp Cys His Arg Asn
65 70 75 80

Leu Asp Pro Ser Glu Thr Ser Leu Lys Pro Asp Glu Leu Ser Leu Leu
85 90 95

Arg Arg Ile Cys Asp Ala Tyr Tyr Leu Pro Asp Trp Cys Ser Pro Ser
100 105 110

Asp Tyr Val Asn Ile Ala Lys Ser Leu Ser Leu Glu Asp Ile Lys Thr
115 120 125

Ala Asp Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Lys
130 135 140

Ser Ala Leu Thr Trp Lys Gly Phe Thr Ser Leu Leu Thr Thr Gly Trp
145 150 155 160

Lys Thr Ile Arg Gly Ala Met Val Met Pro Leu Met Ile Gln Gly Tyr
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gatgagctga atctcctgaa aaggatatgc gatgcatatt atctcccaga ctggtgctct 180
ccttctgatt atgtcaaaat tgccgagtca ctgtctcttg aggatataag gacagctgat 240
tggtcaagag aacgtcgccc caatccggnc tgcnggttat taaatnaagc aattgacatg 300
gnaagggtta actttctcct ggctaagaan tgggtgggaa gacgattaag aaggtggaat 360
gggtgatgcc tccggatgat nnaaggntac aaagaaangg gtcaacaaat ttaacaanaa 420
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20 25 30

Pro Ser Glu Glu Ser Leu Lys Pro Asp Glu Leu Asn Leu Leu Lys Arg
35 40 45

Ile Cys Asp Ala Tyr Tyr Leu Pro Asp Trp Cys Ser Pro Ser Asp Tyr
50 55 60

Val Lys Ile Ala Glu Ser Leu Ser Leu Glu Asp Ile Arg Thr Ala Asp
65 70 75 80

Trp Ser

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gccgcctccc cgatgatcgg agaagaacca aaatgtattg atttggtgtg gattggtggt 480
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20 25 30

Arg Cys Thr Ser Arg His Leu Cys Ala Ser Ala Ser Pro Arg Ala Gly
35 40 45

Leu Cys Leu His His His Arg Arg Arg Arg Arg Ser Ser Arg Arg Thr
50 55 60

Lys Leu Ala Val Arg Ala Met Ala Pro Thr Leu Ser Ser Ser Ser Thr
65 70 75 80

Ala Ala Ala Ala Pro Pro Gly Leu Lys Glu Gly Ile Ala Gly Leu Tyr
85 90 95

Asp Glu Xaa Ser Gly Val Trp Glu Ser Ile Trp Gly Glu His Met His
100 105 110

His Gly Phe Tyr Asp Ala Gly Glu Gly Ala Ser Met Ser Asp His Arg
115 120 125

Arg Ala Pro Val Arg Met Ile Glu Asp Leu Ala Phe Ala Ala Ser Pro
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<212> DNA
<213> Glycine max

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ttcgggcatc ggcagcgagc tcggagagag gggagatagt attggagcag aagccgaaga 180
aggatgacaa gaagaagctg cagaagggaa tcgcagagtt ttacgacgag tcgtctggct 240
tatgggagaa catttggggc gaccacatgc accatggctt ttatgactcg gattccactg 300
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atgcatatta cctccctgcc tggtgctcaa cttctgatta tgttaagttg ctccaatccc 840
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tacaagaaaa tatcttttat atatataaat gattcaatca aattacttga tgaggattat 1200
gagtgaaaat gagaggacag tcatagaaac tttatcctac attccttcta tttccacttc 1260
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aaaaaaaaaa a 1331

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Pro Arg Ser Trp Ala Pro Ile Arg Ala Ser Ala Ala Ser Ser Glu Arg
35 40 45

Gly Glu Ile Val Leu Glu Gln Lys Pro Lys Lys Asp Asp Lys Lys Lys
50 55 60

Leu Gln Lys Gly Ile Ala Glu Phe Tyr Asp Glu Ser Ser Gly Leu Trp

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 65                  70                  75                  80

Glu Asn Ile Trp Gly Asp His Met His His Gly Phe Tyr Asp Ser Asp
                 85                  90                  95

Ser Thr Val Ser Leu Ser Asp His Arg Ala Ala Gln Ile Arg Met Ile
            100                 105                 110

Gln Glu Ser Leu Arg Phe Ala Ser Val Ser Glu Glu Arg Ser Lys Trp
        115                 120                 125

Pro Lys Ser Ile Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg
    130                 135                 140

Tyr Leu Ala Lys Lys Phe Gly Ala Thr Ser Val Gly Ile Thr Leu Ser
145                 150                 155                 160

Pro Val Gln Ala Gln Arg Ala Asn Ala Leu Ala Ala Ala Gln Gly Leu
                165                 170                 175

Ala Asp Lys Val Ser Phe Gln Val Ala Asp Ala Leu Gln Gln Pro Phe
            180                 185                 190

Ser Asp Gly Gln Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His
        195                 200                 205

Met Pro Asp Lys Ala Lys Phe Val Gly Glu Leu Ala Arg Val Ala Ala
    210                 215                 220

Pro Gly Ala Ile Ile Ile Ile Val Thr Trp Cys His Arg Asp Leu Gly
225                 230                 235                 240

Pro Asp Glu Gln Ser Leu His Pro Trp Glu Gln Asp Leu Leu Lys Lys
                245                 250                 255

Ile Cys Asp Ala Tyr Tyr Leu Pro Ala Trp Cys Ser Thr Ser Asp Tyr
            260                 265                 270

Val Lys Leu Leu Gln Ser Leu Ser Leu Gln Asp Ile Lys Ser Glu Asp
        275                 280                 285

Trp Ser Arg Phe Val Ala Pro Phe Trp Pro Ala Val Ile Arg Ser Ala
    290                 295                 300

Phe Thr Trp Lys Gly Leu Ser Ser Leu Leu Ser Ser Gly Lys Leu Gly
305                 310                 315                 320

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aagattgccg agtcattgtc tcttgaggat atcaaaacgg ccgactggtc tgaaaacgtg 660
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tacaagaaag gcctcattaa gttcaagcat catcacctgc cacaaacccc aagcagccat 840
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atagactcng cttgctgtcg ccttggtagc tgaataattc gtgttaccgt gcctctgtat 960
ctgcaactgg aagtgccata tgagaatggt tcctaaaagc aaaatctcct c 1011

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<213> Triticum aestivum

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20 25 30

Ala Gln Ile Arg Met Ile Glu Glu Ala Leu Ala Phe Ala Ala Val Pro
35 40 45

Asp Asp Pro Thr Asn Lys Pro Lys Thr Ile Val Asp Val Gly Cys Gly
50 55 60

Ile Gly Gly Ser Ser Arg Tyr Leu Gly Glu Gln Ile Trp Ser Thr Met
65 70 75 80

Leu Trp Asp His Ile Asp Pro Val Gln Ala Glu Arg Gly Asn Ala Leu
85 90 95

Ala Ala Ala Gln Gly Val Val Arg Thr Arg Phe Phe Pro Ile Ala Asp

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Leu Trp Glu Gln Pro Phe Pro Gly Trp Ala Phe Asp Leu Val Xaa Xaa
        115                 120                 125

Xaa Xaa Xaa Xaa Xaa His Met Pro Asn Lys Gln Lys Phe Val Ser Glu
    130                 135                 140

Leu Ala Arg Val Ala Ala Pro Gly Ala Thr Ile Ile Ile Val Thr Trp
145                 150                 155                 160

Cys His Arg Asn Leu Ala Pro Ser Glu Asp Ser Leu Lys Pro Asp Glu
                165                 170                 175

Leu Asn Leu Leu Lys Lys Ile Cys Asp Ala Tyr Tyr Leu Pro Asp Trp
            180                 185                 190

Cys Ser Pro Ser Asp Tyr Val Lys Ile Ala Glu Ser Leu Ser Leu Glu
        195                 200                 205

Asp Ile Lys Thr Ala Asp Trp Ser Glu Asn Val Ala Pro Phe Trp Pro
    210                 215                 220

Ala Val Ile Gln Ser Ala Leu Thr Trp Lys Gly Leu Thr Ser Leu Leu
225                 230                 235                 240

Arg Ser Gly Trp Lys Thr Ile Lys Gly Ala Leu Val Met Pro Leu Met
                245                 250                 255

Ile Gln Gly Tyr Lys Lys Gly Leu Ile Lys Phe Lys His His His Leu
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Pro Gln Thr Pro Ser Ser His Arg Arg Arg Thr Trp Arg Pro His Arg
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Pro Arg Val Val Glu
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<213> Oryza sativa

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Gly Asn Ser Ala His Ala Ser Leu Leu Leu Arg Ser Ala Ser Val Ala
35 40 45

Phe Leu Phe Thr Ala Pro Tyr Gly Gly Asp His Gly Val Gly Ala Asp
50 55 60

Ala Ala Thr Thr Ala Ser Ile Pro Ser Phe Ser
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ggacgtgggc accgccgaga gcggcctcaa ctcggtggtg ctcgccaaca acgcggagac 180
cgtgctgctg ccgctcaacg agccggtgca cggcaccaag cggcggagcc agatacagac 240
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gctcgggacg ctganggaga tgccnggcgc ctccgcatgg gcggttcgat tcttgggccc 360
gccgccgcca actactacga cggctgcgcg gcgcnccggg acttctctcg ggagagcaat 420
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cattgaanag nnactttctg gngagatcaa gatggtgatg aaagtnaatg gaagntncaa 540
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<220>
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<223> Xaa = ANY AMINO ACID

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Ala Pro Val Ala Ala Tyr Ile Ser Gly Phe Thr Gly Phe His Glu Phe
20 25 30

Ala Glu Phe Thr Ala Glu Asp Val Gly Thr Ala Glu Ser Gly Leu Asn
35 40 45

Ser Val Val Leu Ala Asn Asn Ala Glu Thr Val Leu Leu Pro Leu Asn
50 55 60

Glu Pro Val His Gly Thr Lys Arg Arg Ser Gln Ile Gln Thr Tyr Leu
65 70 75 80

Asp His His Gly Gly Pro Gly Val Gln His Ile Ala Leu Ala Ser Asp
85 90 95

Asp Val Leu Gly Thr Leu Xaa Glu Met Pro Gly Ala Ser Ala Trp Ala
100 105 110

Val Arg Phe Leu Gly Pro Pro Pro Thr Thr
115 120

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<223> n= a, c, g, or t

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<223> n= a, c, g, or t

<400> 15
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taagtcggac cgctttcaag tcaaccgctt ccaccacatc gagttctggt gcaccgatgc 180
caccaacgcc tctcgccgat tctcttgggg acttggaatg cctattgtgg caaaatctga 240
tctctccacc ggaaaccaaa tccacgcctc ctacctcctc cgctccggcg acctctcctt 300
cctcttctcc gctccttact ctccctctct ctccgccggc tcctccgctg cctcctccgc 360
ctccattccc agtttcgacg ccgccacctg ccttgccttc gctgccaaac acggcttcgg 420
cgtccgcgcc atcgccttgg aagtcgccga cgcggaagcc gctttcagcg ccagcgtcgc 480
gaaaggagcc gagccggcgt cgccgccggt tctcgtcgac gatcgcaccg gcttcgcgga 540
ggtgcgcctc tacggcgacg tggtgctccg ctacgtcagc tacaaggacg ccgcgccgca 600
ggcgccacac gcagatncgt cgcggtggtt cctgccggga ttcgaggccg cggcgtcgtc 660
gtcttcgttt ccggagctgg actacgggat ccggcggctg gaccacgccg tcgggaacgt 720
tccggagctg gcgccggcgg tgaggtacct gaaaggcttc agcggattcc acgagttcgc 780
ggagttcacc gcggaggacg tgggaacgag cgagagcggg ttgaactcng tggttctggc 840
ngaacaactc ggagacggtg ttgctgccgc tgaacnagcc cggtttacgg aacgaaagag 900
gaagaagcca nattgagnnc gtatttngaa cacaancnaa aggtgcttgg tgtgcagcaa 960
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acgtttg 1027

<210> 16
<211> 276
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (202)
<223> Xaa = ANY AMINO ACID

<400> 16
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1 5 10 15

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Ala Gln Ala Gln Pro Gly Phe Lys Leu Val Gly Phe Lys Asn Phe Val
            20                  25                  30

Arg Thr Asn Pro Lys Ser Asp Arg Phe Gln Val Asn Arg Phe His His
        35                  40                  45

Ile Glu Phe Trp Cys Thr Asp Ala Thr Asn Ala Ser Arg Arg Phe Ser
    50                  55                  60

Trp Gly Leu Gly Met Pro Ile Val Ala Lys Ser Asp Leu Ser Thr Gly
65                  70                  75                  80

Asn Gln Ile His Ala Ser Tyr Leu Leu Arg Ser Gly Asp Leu Ser Phe
                85                  90                  95

Leu Phe Ser Ala Pro Tyr Ser Pro Ser Leu Ser Ala Gly Ser Ser Ala
            100                 105                 110

Ala Ser Ser Ala Ser Ile Pro Ser Phe Asp Ala Ala Thr Cys Leu Ala
        115                 120                 125

Phe Ala Ala Lys His Gly Phe Gly Val Arg Ala Ile Ala Leu Glu Val
    130                 135                 140

Ala Asp Ala Glu Ala Ala Phe Ser Ala Ser Val Ala Lys Gly Ala Glu
145                 150                 155                 160

Pro Ala Ser Pro Pro Val Leu Val Asp Asp Arg Thr Gly Phe Ala Glu
                165                 170                 175

Val Arg Leu Tyr Gly Asp Val Val Leu Arg Tyr Val Ser Tyr Lys Asp
            180                 185                 190

Ala Ala Pro Gln Ala Pro His Ala Asp Xaa Ser Arg Trp Phe Leu Pro
        195                 200                 205

Gly Phe Glu Ala Ala Ala Ser Ser Ser Ser Phe Pro Glu Leu Asp Tyr
    210                 215                 220

Gly Ile Arg Arg Leu Asp His Ala Val Gly Asn Val Pro Glu Leu Ala
225                 230                 235                 240

Pro Ala Val Arg Tyr Leu Lys Gly Phe Ser Gly Phe His Glu Phe Ala
                245                 250                 255

Glu Phe Thr Ala Glu Asp Val Gly Thr Ser Glu Ser Gly Leu Asn Ser
            260                 265                 270

Val Val Leu Ala
        275
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<210> 17
<211> 511
<212> DNA
<213> Vernonia mesipifolia

<220>
<221> unsure
<222> (494)
<223> n= a, c, g, or t

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cgctgctcct gtaacccttg gaaacaacga cgtcgtattg tctgaagtta agctttacgg 180
cgatgtcgct ttccggtaca taagttacaa aaatccgaac tatacatctt ccttttgcc 240
cgggttcgag cccgttgaaa agacgtcgtc gttttatgac cttgactacg gtatccgccg 300
tttggaccac gccgtaggaa cgtccctgag cttgcttcgg cagtggacta cgtgaaatca 360
ttcaccggat tccatgagtt cgccgaattc accgcggagg acgtcgggac gagcgagagg 420
gaactgaatt cggtcgtttt agcttgcaac agtgagatgg tcttgattcc gatgaacgag 480
ccggtgtacg gaanaaaagg aagagccaga t 511

<210> 18
<211> 170
<212> PRT
<213> Vernonia mesipifolia

<220>
<221> UNSURE
<222> (165)
<223> Xaa = ANY AMINO ACID

<400> 18
His Thr Asp Cys Arg Asn Phe Thr Ala Ser His Gly Leu Ala Val Arg
1 5 10 15

Ala Ile Ala Ile Glu Val Asp Asp Ala Glu Leu Ala Phe Ser Val Ser
20 25 30

Val Ser His Gly Ala Lys Pro Ser Ala Ala Pro Val Thr Leu Gly Asn
35 40 45

Asn Asp Val Val Leu Ser Glu Val Lys Leu Tyr Gly Asp Val Ala Phe
50 55 60

Arg Tyr Ile Ser Tyr Lys Asn Pro Asn Tyr Thr Ser Ser Phe Leu Pro
65 70 75 80

Gly Phe Glu Pro Val Glu Lys Thr Ser Ser Phe Tyr Asp Leu Asp Tyr
85 90 95

Gly Ile Arg Arg Leu Asp His Ala Val Gly Asn Val Pro Glu Leu Ala
100 105 110

Ser Ala Val Asp Tyr Val Lys Ser Phe Thr Gly Phe His Glu Phe Ala
115 120 125

Glu Phe Thr Ala Glu Asp Val Gly Thr Ser Glu Arg Glu Leu Asn Ser
130 135 140

Val Val Leu Ala Cys Asn Ser Glu Met Val Leu Ile Pro Met Asn Glu
145 150 155 160

Pro Val Tyr Gly Xaa Lys Gly Arg Ala Arg
165 170

<210> 19
<211> 1165
<212> DNA
<213> Triticum aestivum

<220>

<221> unsure
<222> (567)
<223> n= a, c, g, or t

<220>
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<222> (596)
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<220>
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<222> (627)
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<222> (697)
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<222> (1039)
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<222> (1126)
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<222> (1152)
<223> n= a, c, g, or t

<400> 19
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ccgcttccac acgctcgcct tccaccacgt cgagttctgg tgcgcggacg ccgcctccgc 180
cgccggccgc ttcgccttcg cgctcggcgc gccgctcgcc gccaggtccg acctctccac 240
ggggaactcc gtgcacgcct cccagctgct ccgctcgggc aacctcgcct tcctcttcac 300
cgcgccctac gccaacggct gcgacgccgc caccgcctcc ctgccctcct tctccgccga 360

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cgccgcgcgc cggttctccg cggaccacgg gctcgcggtg cgctccatag cgctgcgcgt  420
cgcggacgcc gccgaggcct tccgcgccag cgtcgacggg ggcgcgcgcc cggccttcag  480
ccccgtggac ctcggccgcg gcttcggctt tgcggaggtc gagctctacg gcgacgtcgt  540
gctccgcttc gtcagcatcc ggacggnacg gacgtgcctt cttgccgggg ttcganggcg  600
ttgagcaacc gggtgccgtg gactaanggc tgacacggnt tgacacgttg tccgnaagtc  660
cggagcttgc ttcggcgccg cctaacgtag ccggctnaac gggttcaana attcgccagt  720
taacacggag gacgtgggca cggccgagag cgggctcaac tcgatggtgc tcgccaacaa  780
ctcggagggc gtgctgctgc cgctcaacga gccggtgcac ggcaccaagc gccggagcca  840
gatacagacg ttcctggaac accacggcgg ctcgggcgtg cagcacatcg cggtggccag  900
cagcgacgtg ctcaggacgc tcagggagat gcgtgcgcgc tccgccatgg gcggcttcga  960
cttcctgcca cccccgctgc cgaagtacta cgaaggcgtg cggcgcatcg ccggggatgt 1020
gctctcggag gcgcaaatna aggaatgcaa gaactggggg tgctcntcca caaggaagaa 1080
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agatattcac angatctggt gcatg                                      1165
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<210> 20
<211> 179
<212> PRT
<213> Triticum aestivum

<400> 20

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Met Pro Pro Thr Pro Thr Thr Pro Ala Ala Thr Gly Ala Ala Ala Val
  1               5                  10                  15

Thr Pro Glu His Ala Arg Pro Arg Arg Met Val Arg Phe Asn Pro Arg
             20                  25                  30

Ser Asp Arg Phe His Thr Leu Ala Phe His His Val Glu Phe Trp Cys
         35                  40                  45

Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala Leu Gly Ala
     50                  55                  60

Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser Val His Ala
 65                  70                  75                  80

Ser Gln Leu Leu Arg Ser Gly Asn Leu Ala Phe Leu Phe Thr Ala Pro
                 85                  90                  95

Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro Ser Phe Ser
            100                 105                 110

Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Leu Ala Val Arg
        115                 120                 125

Ser Ile Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe Arg Ala Ser
    130                 135                 140

Val Asp Gly Gly Ala Arg Pro Ala Phe Ser Pro Val Asp Leu Gly Arg
145                 150                 155                 160

Gly Phe Gly Phe Ala Glu Val Glu Leu Tyr Gly Asp Val Val Leu Arg
                165                 170                 175

Phe Val Ser
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<210> 21
<211> 1102
<212> DNA
<213> Zea mays

<220>
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<222> (454)
<223> n = a, c, g, or t

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<222> (1072)
<223> n = a, c, g, or t

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<222> (1083)
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<222> (1092)
<223> n = a, c, g, or t

<220>
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<222> (1100)
<223> n = a, c, g, or t

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gccgtcgtca gcctgcgtcc gatggcctcg tcgacggctc aggcccccgc gacggcgccg 180
ccgggtctga aggagggcat cgcggggctg tacgacgagt cgtcggggct gtgggagaac 240
atctggggcg accacatgca ccacggcttc tacgactcga gcgaggccgc ctccatggcc 300
gatcaccgcc gcgcccagat ccgcatgatc gaggaggcgc tcgccttcgc cggtgtccca 360
gcctcagatg atccagagaa gacaccaaaa acaatagtcg atgtcggatg tggcattggt 420
ggtagctcaa ggtacttggc gaagaaatac ggancgcagt gcactgggat cacgttgagc 480
cctgttcaag ccgagagagg aaatgctctc gctgcagcgc aggggttgtc ggatcaggtt 540
actctgcaag ttgctgatgc tctggagcaa ccgtttcctg acgggcagtt cgatctggtg 600
tggtccatgg agagtggcga gcacatgccg gacaagagaa agtttgttag tgagctagca 660
cgcgtggcgg ctcctggagg gacaataatc atcgtgacat ggtgccatag gaacctggat 720
ccatccgaaa cctcgctaaa gcccgatgaa ctgagcctcc tgaggaggat atgcgacgcg 780
tactacctcc cggactggtg ctcaccttca gactatgtga acattgccaa gtcactgtct 840
ctcgaggata tcaagacagc tgactggtcg gagaacgtgg ccccgttttg gcccgccgtg 900
ataaaatcag cgctaacatg gaagggcttc acctctctgc tgacgaccgg atggaagacg 960
atcagaggcg cgatggtgat gccgctaatg atccagggct acaagaaggg gctcatcaaa 1020
ttcaccatca tcacctgtcg caagcctgga gccgcgtagt gatctatacc gnccacggcg 1080
tcnttaactc tnacggaaan ct 1102

<210> 22
<211> 352
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (152)
<223> Xaa = ANY AMINO ACID

<400> 22
Met Ala His Ala Ala Leu Leu His Cys Ser Gln Ser Ser Arg Ser Leu
1 5 10 15

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Ala Ala Cys Arg Arg Gly Ser His Tyr Arg Ala Pro Ser His Val Pro
            20                  25                  30

Arg His Ser Arg Arg Leu Arg Arg Ala Val Val Ser Leu Arg Pro Met
        35                  40                  45

Ala Ser Ser Thr Ala Gln Ala Pro Ala Thr Ala Pro Pro Gly Leu Lys
    50                  55                  60

Glu Gly Ile Ala Gly Leu Tyr Asp Glu Ser Ser Gly Leu Trp Glu Asn
65                  70                  75                  80

Ile Trp Gly Asp His Met His His Gly Phe Tyr Asp Ser Ser Glu Ala
                85                  90                  95

Ala Ser Met Ala Asp His Arg Arg Ala Gln Ile Arg Met Ile Glu Glu
            100                 105                 110

Ala Leu Ala Phe Ala Gly Val Pro Ala Ser Asp Asp Pro Glu Lys Thr
        115                 120                 125

Pro Lys Thr Ile Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg
    130                 135                 140

Tyr Leu Ala Lys Lys Tyr Gly Xaa Gln Cys Thr Gly Ile Thr Leu Ser
145                 150                 155                 160

Pro Val Gln Ala Glu Arg Gly Asn Ala Leu Ala Ala Ala Gln Gly Leu
                165                 170                 175

Ser Asp Gln Val Thr Leu Gln Val Ala Asp Ala Leu Glu Gln Pro Phe
            180                 185                 190

Pro Asp Gly Gln Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His
        195                 200                 205

Met Pro Asp Lys Arg Lys Phe Val Ser Glu Leu Ala Arg Val Ala Ala
    210                 215                 220

Pro Gly Gly Thr Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Asp
225                 230                 235                 240

Pro Ser Glu Thr Ser Leu Lys Pro Asp Glu Leu Ser Leu Leu Arg Arg
                245                 250                 255

Ile Cys Asp Ala Tyr Tyr Leu Pro Asp Trp Cys Ser Pro Ser Asp Tyr
            260                 265                 270

Val Asn Ile Ala Lys Ser Leu Ser Leu Glu Asp Ile Lys Thr Ala Asp
        275                 280                 285

Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Lys Ser Ala
    290                 295                 300

Leu Thr Trp Lys Gly Phe Thr Ser Leu Leu Thr Thr Gly Trp Lys Thr
305                 310                 315                 320

Ile Arg Gly Ala Met Val Met Pro Leu Met Ile Gln Gly Tyr Lys Lys
                325                 330                 335

Gly Leu Ile Lys Phe Thr Ile Ile Thr Cys Arg Lys Pro Gly Ala Ala
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340 345 350

<210> 23
<211> 521
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (269)
<223> n = a, c, g, or t

<220>
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<222> (274)
<223> n = a, c, g, or t

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<222> (286)
<223> n = a, c, g, or t

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<222> (302)
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<222> (381)..(382)
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<222> (418)
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<222> (436)
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<222> (473)
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<220>
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<222> (514)
<223> n = a, c, g, or t

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ataatcattg tgacctggtg ccataggaac ctcgagccat ccgaagagtc cctgaaacct 120
gatgagctga atctcctgaa aaggatatgc gatgcatatt atctcccaga ctggtgctct 180
ccttctgatt atgtcaaaat tgccgagtca ctgtctcttg aggatataag gacagctgat 240
tggtcaagag aacgtcgccc caatccggnc tgcnggttat taaatnaagc aattgacatg 300
gnaagggtta actttctcct ggctaagaan tgggtgggaa gacgattaag aaggtggaat 360
gggtgatgcc tccggatgat nnaaggntac aaagaaangg gtcaacaaat ttaacaanaa 420
caacctgtnc caaagncccg aaacaacgca ataatacccc antaatnaaa ttncgctcct 480
ggctaacctt ctccaacaac gaattaatgg aaanttctga c 521

<210> 24
<211> 172
<212> PRT
<213> Oryza sativa

<400> 24
Phe Arg His Gly His Ala Leu Ala Gln Pro Phe Pro Asp Gly Gln Phe
1 5 10 15

Asp Leu Val Trp Ser Met Glu Ser Asp Glu His Met Pro Asp Lys Arg
20 25 30

Gln Phe Val Ser Glu Leu Ala Arg Val Ala Ala Pro Gly Ala Arg Ile
35 40 45

Ile Ile Val Thr Trp Cys His Arg Asn Leu Glu Pro Ser Glu Glu Ser
50 55 60

Leu Lys Pro Asp Glu Leu Asn Leu Leu Lys Arg Ile Cys Asp Ala Tyr
65 70 75 80

Tyr Leu Pro Asp Trp Cys Ser Pro Ser Asp Tyr Val Lys Ile Ala Glu
85 90 95

Ser Leu Ser Leu Glu Asp Ile Arg Thr Ala Asp Trp Ser Glu Asn Val
100 105 110

Ala Pro Phe Trp Pro Ala Val Ile Lys Ser Ala Leu Thr Trp Lys Gly
115 120 125

Leu Thr Ser Leu Leu Arg Ser Gly Trp Glu Thr Val Arg Gly Ala Met
130 135 140

Val Met Pro Leu Val Ile Glu Gly Tyr Lys Lys Gly Leu Ile Lys Phe
145 150 155 160

Pro Ile Ile Thr Cys Arg Lys Pro Glu Thr Thr Gln
165 170

<210> 25
<211> 464
<212> DNA
<213> Oryza sativa

<400> 25
gcacgagtac agcccacggg cgcactggca ccgctgcatc cactgctccg ctgcacgagc 60
cgtcatctct gcgcctcggc ttcccctcgc gccggcctct gcctccacca ccaccgccgc 120
cgccgccgca gcagccggag gacgaaactc gccgtgcgcg cgatggcacc gacgttgtcc 180
tcgtcgtcga cggcggcggc agctcccccg gggctgaagg agggcatcgc ggggctctac 240
gacgagtcgt ccggcgtgtg ggagagcatc tggggcgagc acatgcacca cggcttctac 300
gacgccggcg aggccgcctc catgtccgac caccgccgcg cccagatccg catgatcgag 360
gaatccctcg ccttcgccgc cgttccccga tgatgcgggt aacaaaccca aaagtgttat 420
ttactgtttg gtgttgcaaa tgggggtacc tccaaaaaac tttg 464

<210> 26
<211> 128
<212> PRT
<213> Oryza sativa

<400> 26
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1 5 10 15

Arg Cys Thr Ser Arg His Leu Cys Ala Ser Ala Ser Pro Arg Ala Gly
20 25 30

Leu Cys Leu His His His Arg Arg Arg Arg Arg Ser Ser Arg Arg Thr
35 40 45

Lys Leu Ala Val Arg Ala Met Ala Pro Thr Leu Ser Ser Ser Ser Thr
50 55 60

Ala Ala Ala Ala Pro Pro Gly Leu Lys Glu Gly Ile Ala Gly Leu Tyr
65 70 75 80

Asp Glu Ser Ser Gly Val Trp Glu Ser Ile Trp Gly Glu His Met His
85 90 95

His Gly Phe Tyr Asp Ala Gly Glu Ala Ala Ser Met Ser Asp His Arg
100 105 110

Arg Ala Gln Ile Arg Met Ile Glu Glu Ser Leu Ala Phe Ala Ala Val
115 120 125

<210> 27
<211> 1189
<212> DNA
<213> Glycine max

<400> 27

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ttcccaatcc cctcgcactt tcgccagaat ccgggtcgga cccaggtcgt gggctcctat  120
tcgggcatcg gcagcgagct cggagagagg ggagatagta ttggagcaga agccgaagaa  180
ggatgacaag aagaagctgc agaagggaat cgcagagttt tacgacgagt cgtctggctt  240
atgggagaac atttggggcg accacatgca ccatggcttt tatgactcgg attccactgt  300
ttcgctttcg gatcatcgtg ctgctcagat ccgaatgatc caagagtctc ttcgctttgc  360
ctctgtttct gaggagcgta gtaaatggcc caagagtata gttgatgttg ggtgtggcat  420
aggtggcagc tctagatacc tggccaagaa atttggagca accagtgtag gcatcactct  480
gagtcctgtt caagctcaaa gagcaaatgc tcttgctgct gctcaaggat tggctgataa  540
ggtttccttt caggttgctg acgctctaca gcaaccattc tctgacggcc agtttgatct  600
ggtgtggtcc atggagagtg gagagcatat gcctgacaaa gctaagtttg ttggagagtt  660
agctcgggta gcagcaccag gtgccattat aataatagta acatggtgcc acagggatct  720
tggccctgac gaacaatcct tacatccatg ggagcaagat ctcttaaaga agatttgcga  780
tgcatattac ctccctgcct ggtgctcaac ttctgattat gttaagttgc tccaatccct  840
gtcacttcag gacatcaagt cagaagattg gtctcgcttt gttgctccat tttggccagc  900
agtgatacgc tcagccttca catggaaggg tctatcttca ctcttgagca gtggacaaaa  960
aacgataaaa ggagctttgg ctatgccatt gatgatagag ggatacaaga aagatctaat 1020
taagtttgcc atcattacat gtcgaaaacc tgaataaatg gagaggcagg attactttta 1080
tagaatgaac caagtttcca acaggtcgtt tatttcgata gttgagaaac aagagaaaaa 1140
ataaatgaaa ggggttgttc gattttaaaa aaaaaaaaaa aaaaaaaaa              1189
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<210> 28
<211> 350
<212> PRT
<213> Glycine max

<400> 28

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Met Ala Thr Val Val Arg Ile Pro Thr Ile Ser Cys Ile His Ile His
  1               5                  10                  15

Thr Phe Arg Ser Gln Ser Pro Arg Thr Phe Ala Arg Ile Arg Val Gly
             20                  25                  30

Pro Arg Ser Trp Ala Pro Ile Arg Ala Ser Ala Ala Ser Ser Glu Arg
         35                  40                  45

Gly Glu Ile Val Leu Glu Gln Lys Pro Lys Lys Asp Asp Lys Lys Lys
     50                  55                  60

Leu Gln Lys Gly Ile Ala Glu Phe Tyr Asp Glu Ser Ser Gly Leu Trp
 65                  70                  75                  80

Glu Asn Ile Trp Gly Asp His Met His His Gly Phe Tyr Asp Ser Asp
                 85                  90                  95

Ser Thr Val Ser Leu Ser Asp His Arg Ala Ala Gln Ile Arg Met Ile
            100                 105                 110

Gln Glu Ser Leu Arg Phe Ala Ser Val Ser Glu Glu Arg Ser Lys Trp
        115                 120                 125

Pro Lys Ser Ile Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg
    130                 135                 140

Tyr Leu Ala Lys Lys Phe Gly Ala Thr Ser Val Gly Ile Thr Leu Ser
145                 150                 155                 160

Pro Val Gln Ala Gln Arg Ala Asn Ala Leu Ala Ala Ala Gln Gly Leu
                165                 170                 175

Ala Asp Lys Val Ser Phe Gln Val Ala Asp Ala Leu Gln Gln Pro Phe
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Ser Asp Gly Gln Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His
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Met Pro Asp Lys Ala Lys Phe Val Gly Glu Leu Ala Arg Val Ala Ala
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Pro Gly Ala Ile Ile Ile Ile Val Thr Trp Cys His Arg Asp Leu Gly
225                 230                 235                 240

Pro Asp Glu Gln Ser Leu His Pro Trp Glu Gln Asp Leu Leu Lys Lys
                245                 250                 255

Ile Cys Asp Ala Tyr Tyr Leu Pro Ala Trp Cys Ser Thr Ser Asp Tyr
            260                 265                 270

Val Lys Leu Leu Gln Ser Leu Ser Leu Gln Asp Ile Lys Ser Glu Asp
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Trp Ser Arg Phe Val Ala Pro Phe Trp Pro Ala Val Ile Arg Ser Ala
    290                 295                 300

Phe Thr Trp Lys Gly Leu Ser Ser Leu Leu Ser Ser Gly Gln Lys Thr
305                 310                 315                 320

Ile Lys Gly Ala Leu Ala Met Pro Leu Met Ile Glu Gly Tyr Lys Lys
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Asp Leu Ile Lys Phe Ala Ile Ile Thr Cys Arg Lys Pro Glu
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